

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/800,187

DATE: 10/29/2001

TIME: 15:13:38

Input Set : A:\Huv03701.app

Output Set: N:\CRF3\10292001\I800187.raw

3 <110> APPLICANT: GROZINGER, CHRISTINA M.
4 HASSIG, CHRISTIAN A.
5 SCHREIBER, STUART L.
7 <120> TITLE OF INVENTION: CLASS II HUMAN HISTONE DEACETYLASES, AND USES RELATED
8 THERETO
10 <130> FILE REFERENCE: HUV-037.01
12 <140> CURRENT APPLICATION NUMBER: 09/800,187
13 <141> CURRENT FILING DATE: 2001-03-05
15 <150> PRIOR APPLICATION NUMBER: 60/186,802
16 <151> PRIOR FILING DATE: 2000-03-03
18 <160> NUMBER OF SEQ ID NOS: 73
20 <170> SOFTWARE: PatentIn Ver. 2.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 3255
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
27 <400> SEQUENCE: 1

ENTERED

P.5

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57 cgccagccca gtgagcagga gctgctcttc agacagcaag ccctcctgct ggagcagcag 1800

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58 cggatccacc agctgaggaa ctaccaggcg tccatggagg ccgcccggcat ccccggtgtcc 1860
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86 <211> LENGTH: 1084

87 <212> TYPE: PRT

88 <213> ORGANISM: Homo sapiens

90 <400> SEQUENCE: 2

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94 Val Glu Leu Leu Asn Pro Ala Arg Val Asn His Met Pro Ser Thr Val
95 20 25 30
97 Asp Val Ala Thr Ala Leu Pro Leu Gln Val Ala Pro Ser Ala Val Pro
98 35 40 45
100 Met Asp Leu Arg Leu Asp His Gln Phe Ser Leu Pro Val Ala Glu Pro
101 50 55 60
103 Ala Leu Arg Glu Gln Gln Leu Gln Gln Glu Leu Leu Ala Leu Lys Gln
104 65 70 75 80
106 Lys Gln Gln Ile Gln Arg Gln Ile Leu Ile Ala Glu Phe Gln Arg Gln
107 85 90 95
109 His Glu Gln Leu Ser Arg Gln His Glu Ala Gln Leu His Glu His Ile
110 100 105 110
112 Lys Gln Gln Gln Glu Met Leu Ala Met Lys His Gln Gln Glu Leu Leu
113 115 120 125
115 Glu His Gln Arg Lys Leu Glu Arg His Arg Gln Glu Gln Glu Leu Glu
116 130 135 140
118 Lys Gln His Arg Glu Gln Lys Leu Gln Gln Leu Lys Asn Lys Glu Lys

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119	145				150				155				160			
121	Gly	Lys	Glu	Ser	Ala	Val	Ala	Ser	Thr	Glu	Val	Lys	Met	Lys	Leu	Gln
122					165				170						175	
124	Glu	Phe	Val	Leu	Asn	Lys	Lys	Lys	Ala	Leu	Ala	His	Arg	Asn	Leu	Asn
125					180				185						190	
127	His	Cys	Ile	Ser	Ser	Asp	Pro	Arg	Tyr	Trp	Tyr	Gly	Lys	Thr	Gln	His
128					195				200					205		
130	Ser	Ser	Leu	Asp	Gln	Ser	Ser	Pro	Pro	Gln	Ser	Gly	Val	Ser	Thr	Ser
131		210					215						220			
133	Tyr	Asn	His	Pro	Val	Leu	Gly	Met	Tyr	Asp	Ala	Lys	Asp	Asp	Phe	Pro
134	225					230					235					240
136	Leu	Arg	Lys	Thr	Ala	Ser	Glu	Pro	Asn	Leu	Lys	Leu	Arg	Ser	Arg	Leu
137					245				250							255
139	Lys	Gln	Lys	Val	Ala	Glu	Arg	Arg	Ser	Ser	Pro	Leu	Leu	Arg	Arg	Lys
140					260				265						270	
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143					275				280					285		
145	Asp	Ser	Ala	Cys	Ser	Ser	Ala	Pro	Gly	Ser	Gly	Pro	Ser	Ser	Pro	Asn
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148	Asn	Ser	Ser	Gly	Ser	Val	Ser	Ala	Glu	Asn	Gly	Ile	Ala	Pro	Ala	Val
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151	Pro	Ser	Ile	Pro	Ala	Glu	Thr	Ser	Leu	Ala	His	Arg	Leu	Val	Ala	Arg
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154	Glu	Gly	Ser	Ala	Ala	Pro	Leu	Pro	Leu	Tyr	Thr	Ser	Pro	Ser	Leu	Pro
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163	Leu	Ser	Leu	Phe	Pro	Gly	Thr	His	Leu	Thr	Pro	Tyr	Leu	Ser	Thr	Ser
164	385					390					395					400
166	Pro	Leu	Glu	Arg	Asp	Gly	Gly	Ala	Ala	His	Ser	Pro	Leu	Leu	Gln	His
167					405					410					415	
169	Met	Val	Leu	Leu	Glu	Gln	Pro	Pro	Ala	Gln	Ala	Pro	Leu	Val	Thr	Gly
170					420				425					430		
172	Leu	Gly	Ala	Leu	Pro	Leu	His	Ala	Gln	Ser	Leu	Val	Gly	Ala	Asp	Arg
173			435					440					445			
175	Val	Ser	Pro	Ser	Ile	His	Lys	Leu	Arg	Gln	His	Arg	Pro	Leu	Gly	Arg
176		450					455					460				
178	Thr	Gln	Ser	Ala	Pro	Leu	Pro	Gln	Asn	Ala	Gln	Ala	Leu	Gln	His	Leu
179	465					470					475					480
181	Val	Ile	Gln	Gln	Gln	His	Gln	Gln	Phe	Leu	Glu	Lys	His	Lys	Gln	Gln
182					485					490					495	
184	Phe	Gln	Gln	Gln	Gln	Leu	Gln	Met	Asn	Lys	Ile	Ile	Pro	Lys	Pro	Ser
185					500				505					510		
187	Glu	Pro	Ala	Arg	Gln	Pro	Glu	Ser	His	Pro	Glu	Glu	Thr	Glu	Glu	Glu
188			515					520					525			
190	Leu	Arg	Glu	His	Gln	Ala	Leu	Leu	Asp	Glu	Pro	Tyr	Leu	Asp	Arg	Leu
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194 545                    550                    555                    560
196 Glu Pro Ile Glu Ser Asp Glu Glu Glu Ala Glu Pro Pro Arg Glu Val
197                    565                    570                    575
199 Glu Pro Gly Gln Arg Gln Pro Ser Glu Gln Glu Leu Leu Phe Arg Gln
200                    580                    585                    590
202 Gln Ala Leu Leu Glu Gln Gln Arg Ile His Gln Leu Arg Asn Tyr
203                    595                    600                    605
205 Gln Ala Ser Met Glu Ala Ala Gly Ile Pro Val Ser Phe Gly Gly His
206                    610                    615                    620
208 Arg Pro Leu Ser Arg Ala Gln Ser Ser Pro Ala Ser Ala Thr Phe Pro
209 625                    630                    635                    640
211 Val Ser Val Gln Glu Pro Pro Thr Lys Pro Arg Phe Thr Thr Gly Leu
212                    645                    650                    655
214 Val Tyr Asp Thr Leu Met Leu Lys His Gln Cys Thr Cys Gly Ser Ser
215                    660                    665                    670
217 Ser Ser His Pro Glu His Ala Gly Arg Ile Gln Ser Ile Trp Ser Arg
218                    675                    680                    685
220 Leu Gln Glu Thr Gly Leu Arg Gly Lys Cys Glu Cys Ile Arg Gly Arg
221                    690                    695                    700
223 Lys Ala Thr Leu Glu Glu Leu Gln Thr Val His Ser Glu Ala His Thr
224 705                    710                    715                    720
226 Leu Leu Tyr Gly Thr Asn Pro Leu Asn Arg Gln Lys Leu Asp Ser Lys
227                    725                    730                    735
229 Lys Leu Leu Gly Ser Leu Ala Ser Val Phe Val Arg Leu Pro Cys Gly
230                    740                    745                    750
232 Gly Val Gly Val Asp Ser Asp Thr Ile Trp Asn Glu Val His Ser Ala
233                    755                    760                    765
235 Gly Ala Ala Arg Leu Ala Val Gly Cys Val Val Glu Leu Val Phe Lys
236                    770                    775                    780
238 Val Ala Thr Gly Glu Leu Lys Asn Gly Phe Ala Val Val Arg Pro Pro
239 785                    790                    795                    800
241 Gly His His Ala Glu Glu Ser Thr Pro Met Gly Phe Cys Tyr Phe Asn
242                    805                    810                    815
244 Ser Val Ala Val Ala Ala Lys Leu Leu Gln Gln Arg Leu Ser Val Ser
245                    820                    825                    830
247 Lys Ile Leu Ile Val Asp Trp Asp Val His His Gly Asn Gly Thr Gln
248                    835                    840                    845
250 Gln Ala Phe Tyr Ser Asp Pro Ser Val Leu Tyr Met Ser Leu His Arg
251                    850                    855                    860
253 Tyr Asp Asp Gly Asn Phe Phe Pro Gly Ser Gly Ala Pro Asp Glu Val
254 865                    870                    875                    880
256 Gly Thr Gly Pro Gly Val Gly Phe Asn Val Asn Met Ala Phe Thr Gly
257                    885                    890                    895
259 Gly Leu Asp Pro Pro Met Gly Asp Ala Glu Tyr Leu Ala Ala Phe Arg
260                    900                    905                    910
262 Thr Val Val Met Pro Ile Ala Ser Glu Phe Ala Pro Asp Val Val Leu
263                    915                    920                    925
265 Val Ser Ser Gly Phe Asp Ala Val Glu Gly His Pro Thr Pro Leu Gly

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268 Gly Tyr Asn Leu Ser Ala Arg Cys Phe Gly Tyr Leu Thr Lys Gln Leu
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272      965      970      975
274 Asp Leu Thr Ala Ile Cys Asp Ala Ser Glu Ala Cys Val Ser Ala Leu
275      980      985      990
277 Leu Gly Asn Glu Leu Asp Pro Leu Pro Glu Lys Val Leu Gln Gln Arg
278      995      1000      1005
280 Pro Asn Ala Asn Ala Val Arg Ser Met Glu Lys Val Met Glu Ile His
281      1010      1015      1020
283 Ser Lys Tyr Trp Arg Cys Leu Gln Arg Thr Thr Ser Thr Ala Gly Arg
284 1025      1030      1035      1040
286 Ser Leu Ile Glu Ala Gln Thr Cys Glu Asn Glu Glu Ala Glu Thr Val
287      1045      1050      1055
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290      1060      1065      1070
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296 <210> SEQ ID NO: 3
297 <211> LENGTH: 3369
298 <212> TYPE: DNA
299 <213> ORGANISM: Homo sapiens
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308 caggagatgc tggcagccaa gcagcagcag gagatgctgg cagccaagcg gcagcaggag 420
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314 cctttgcctg ggccctacga cagtcgagac gacttcccc tccgcaaaac agcctctgaa 780
315 cccaacttga aagtgcgttc aaggctaaaa cagaaggttg ctgagcggag aagcagtcct 840
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317 acaggtgccg ggctggggc gtcgtccgtg tgtaacagcg caccgggctc cggccccagc 960
318 tctcccaaca gctcccacag caccatcgct gagaatggct ttactggctc agtccccaac 1020
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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:985 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:988 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:991 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1560 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1598 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:1627 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:1656 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:1680 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1719 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1738 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:1757 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25